

INPUT SET: S749.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING  
2

## 3 (1) General Information:

4 (i) APPLICANT: Bucala, Richard J. et al.

5 (ii) TITLE OF INVENTION: Inhibition of Migration Inhibitory  
6 Factor in the Treatment of Diseases Involving  
7 Cytokine-Mediated Toxicity

8 (iii) NUMBER OF SEQUENCES: 17

9 (iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: PENNIE & EDMONDS  
11 (B) STREET: 1155 Avenue of the Americas  
12 (C) CITY: New York  
13 (D) STATE: New York  
14 (E) COUNTRY: U.S.A.  
15 (F) ZIP: 10036-2711

16 (v) COMPUTER READABLE FORM:

17 (A) MEDIUM TYPE: Floppy disk  
18 (B) COMPUTER: IBM PC compatible  
19 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

21 (vi) CURRENT APPLICATION DATA:

22 (A) APPLICATION NUMBER: US 08/243,342  
23 (B) FILING DATE: 16-MAY-1994  
24 (C) CLASSIFICATION:

25 (viii) ATTORNEY/AGENT INFORMATION:

26 (A) NAME: Coruzzi, Laura A.  
27 (B) REGISTRATION NUMBER: 30,742  
28 (C) REFERENCE/DOCKET NUMBER: 7815-008

29 (ix) TELECOMMUNICATION INFORMATION:

30 (A) TELEPHONE: 212 790-9090  
31 (B) TELEFAX: 212 869-8864/9741  
32 (C) TELEX: 66141 PENNIE

33 (2) INFORMATION FOR SEQ ID NO:1:

34 (i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 348 base pairs

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47 (B) TYPE: nucleic acid  
48 (C) STRANDEDNESS: single  
49 (D) TOPOLOGY: unknown  
50  
51 (ii) MOLECULE TYPE: DNA  
52  
53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
54  
55 ATGCCTATGT TCATCGTGAA CACCAATGTT CCCCCGCCCT CCGTGCCAGA GGGGTTCTG 60  
56  
57 TCGGAGCTCA CCCAGCAGCT GGCGCAGGCC ACCGGCAAGC CCGCACAGTA CATCGCAGTG 120  
58  
59 CACGTGGTCC CGGACCAGCT CATGACTTTT AGCGGCACGA ACGATCCCTG CGCCCTCTGC 180  
60  
61 AGCCTGCACA GCATCGGCAA GATCGGTGGT GCCCAGAACC GCAACTACAG TAAGCTGCTG 240  
62  
63 TGTGGCCTGC TGTCCGATCG CCTGCACATC AGCCCGGACC GGGTCTACAT CAACTATTAC 300  
64  
65 GACATGAACG CTGCCAACGT GGGCTGGAAC GGTTCCACCT TCGCTTGA 348  
66  
67  
68 (2) INFORMATION FOR SEQ ID NO:2:  
69  
70 (i) SEQUENCE CHARACTERISTICS:  
71 (A) LENGTH: 348 base pairs  
72 (B) TYPE: nucleic acid  
73 (C) STRANDEDNESS: single  
74 (D) TOPOLOGY: unknown  
75  
76 (ii) MOLECULE TYPE: DNA  
77  
78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
79  
80 ATGCCGATGT TCATCGTAAA CACCAACGTG CCCCCGCCCT CCGTGCCGGA CGGGTTCCCTC 60  
81  
82 TCCGAGCTCA CCCAGCAGCT GGCGCAGGCC ACCGGCAAGC CCCCCCAGTA CATCGCGGTG 120  
83  
84 CACGTGGTCC CGGACCAGCT CATGGCCTTC GGCGGCTCCA GCGAGCCGTG CGCGCTCTGC 180  
85  
86 AGCCTGCACA GCATCGGCAA GATCGGCAGC GCGCAGAACC GCTCCTACAG CAAGCTGCTG 240  
87  
88 TGCGGCCTGC TGGCCGAGCG CCTGCCATC AGCCCGGACA GGGTCTACAT CAACTATTAC 300  
89  
90 GACATGAACG CGGCCAGTGT GGGCTGGAAC AACTCCACCT TCGCCTAA 348  
91  
92  
93 (2) INFORMATION FOR SEQ ID NO:3:  
94  
95 (i) SEQUENCE CHARACTERISTICS:  
96 (A) LENGTH: 501 base pairs  
97 (B) TYPE: nucleic acid  
98 (C) STRANDEDNESS: single  
99 (D) TOPOLOGY: unknown

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/243,342DATE: 11/01/94  
TIME: 16:45:37

INPUT SET: S749.raw

100  
101 (ii) MOLECULE TYPE: cDNA  
102  
103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
104  
105 CCATGCCTAT GTTCATCGTG AACACCAATG TTCCCCGCGC CTCCGTGCCA GAGGGGTTTC 60  
106  
107 TGTCGGAGCT CACCCAGCAG CTGGCGCAGG CCACCGGCAA GCCCGCACAG TACATCGCAG 120  
108  
109 TGCACGTGGT CCCGGACCAG CTCATGACTT TTAGCGGCAC GAACGATCCC TGCGCCCTCT 180  
110  
111 GCAGCCTGCA CAGCATCGGC AAGATCGGTG GTGCCAGAA CCGCAACTAC AGTAAGCTGC 240  
112  
113 TGTGTGGCCT GCTGTCCGAT CGCCTGCACA TCAGCCCGGA CCGCTCCTAC AGCAAGCTGC 300  
114  
115 TGTGCGGCCT GCTGGCCGAG CGCCTGCGCA TCAGCCCGGA CCGGGTCTAC ATCAACTATT 360  
116  
117 ACGACATGAA CGCTGCCAAC GTGGGCTGGA ACGGTTCCAC CAGGGTCTAC ATCAACTATT 420  
118  
119 ACGACATGAA CGCGGCCAGT GTGGGCTGGA ACAACTCCAC CTTCGCTTGA GTCCTGGCCC 480  
120  
121 CACTTACCTG CACCGCTGTT C 501  
122  
123  
124 (2) INFORMATION FOR SEQ ID NO:4:  
125  
126 (i) SEQUENCE CHARACTERISTICS:  
127 (A) LENGTH: 115 amino acids  
128 (B) TYPE: amino acid  
129 (C) STRANDEDNESS: single  
130 (D) TOPOLOGY: unknown  
131  
132 (ii) MOLECULE TYPE: peptide  
133  
134 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
135  
136 Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro  
137 1 5 10 15  
138  
139 Glu Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly  
140 20 25 30  
141  
142 Lys Pro Ala Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met  
143 35 40 45  
144  
145 Thr Phe Ser Gly Thr Asn Asp Pro Cys Ala Leu Cys Ser Leu His Ser  
146 50 55 60  
147  
148 Ile Gly Lys Ile Gly Gly Ala Gln Asn Arg Asn Tyr Ser Lys Leu Leu  
149 65 70 75 80  
150  
151 Cys Gly Leu Leu Ser Asp Arg Leu His Ile Ser Pro Asp Arg Val Tyr  
152 85 90 95

## INPUT SET: S749.raw

153  
154       Ile Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Gly Ser  
155                   100                   105                   110  
156  
157        Thr Phe Ala  
158                   115  
159  
160  
161 (2) INFORMATION FOR SEQ ID NO:5:  
162

163       (i) SEQUENCE CHARACTERISTICS:  
164           (A) LENGTH: 115 amino acids  
165           (B) TYPE: amino acid  
166           (C) STRANDEDNESS: single  
167           (D) TOPOLOGY: unknown  
168

169       (ii) MOLECULE TYPE: peptide  
170

171       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
172

173       Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro  
174           1                   5                   10                   15  
175

176       Asp Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly  
177                   20                   25                   30  
178

179       Lys Pro Pro Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met  
180                   35                   40                   45  
181

182       Ala Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser  
183                   50                   55                   60  
184

185       Ile Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu  
186                   65                   70                   75                   80  
187

188       Cys Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr  
189                   85                   90                   95  
190

191       Ile Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser  
192                   100                   105                   110  
193

194       Thr Phe Ala  
195                   115  
196  
197

198 (2) INFORMATION FOR SEQ ID NO:6:  
199

200       (i) SEQUENCE CHARACTERISTICS:  
201           (A) LENGTH: 9 amino acids  
202           (B) TYPE: amino acid  
203           (C) STRANDEDNESS: single  
204           (D) TOPOLOGY: unknown  
205

INPUT SET: S749.raw

206 (ii) MOLECULE TYPE: peptide  
207  
208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
209  
210 Ala Lys Lys Gly Ala Val Gly Gly Ile  
211 1 5  
212  
213  
214 (2) INFORMATION FOR SEQ ID NO:7:  
215  
216 (i) SEQUENCE CHARACTERISTICS:  
217 (A) LENGTH: 17 amino acids  
218 (B) TYPE: amino acid  
219 (C) STRANDEDNESS: single  
220 (D) TOPOLOGY: unknown  
221  
222 (ii) MOLECULE TYPE: peptide  
223  
224 (ix) FEATURE:  
225 (A) NAME/KEY: Peptide  
226 (B) LOCATION: 15  
227 (D) OTHER INFORMATION: /label= X  
228 /note= "X = Asn or Gly"  
229  
230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
231  
232 Ile Xaa His Asn Thr Val Ala Thr Glu Ile Ser Gly Tyr Asn Xaa Ala  
233 1 5 10 15  
234  
235 Met  
236  
237  
238 (2) INFORMATION FOR SEQ ID NO:8:  
239  
240 (i) SEQUENCE CHARACTERISTICS:  
241 (A) LENGTH: 27 base pairs  
242 (B) TYPE: nucleic acid  
243 (C) STRANDEDNESS: single  
244 (D) TOPOLOGY: unknown  
245  
246 (ii) MOLECULE TYPE: DNA  
247  
248 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
249  
250 CCATATGCCG ATGTTCATCG TAAACAC 27  
251  
252  
253 (2) INFORMATION FOR SEQ ID NO:9:  
254  
255 (i) SEQUENCE CHARACTERISTICS:  
256 (A) LENGTH: 26 base pairs  
257 (B) TYPE: nucleic acid  
258 (C) STRANDEDNESS: single

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
PATENT APPLICATION **US/08/243,342**

DATE: 11/01/94  
TIME: 16:45:47

***INPUT SET: S749.raw***

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Original Text